Toxicogenomics as a Tool to Assess Exposure of Fish to Environmental Pollutants

Iris Knoebl Biologist NERL (513) 569-7622 knoebl.iris@epa.gov

Key Words: gene arrays, endocrine-disrupting chemicals, fathead minnow, CAFO, gene expression

Molecular biological techniques such as gene arrays and quantitative PCR techniques are becoming important tools to study alterations in normal gene expression in fish and other wildlife exposed to such pollutants as endocrine-disrupting chemicals (EDCs). Gene arrays provide a method to measure a "snapshot" of gene activity at a particular time in response to an exposure, while quantitative PCR is a method to quantitatively measure the activity of particular genes. These tools are being developed and tested by laboratory studies at the Ecological Exposure Research Division of the National Exposure Research Laboratory (EERD/NERL) in Cincinnati. An important function for these tools is the ability to translate from the laboratory to field conditions to assess exposure to EDCs and other pollutants in wild fish. For example, these methods can be used to assess the effect of concentrated animal feeding operation (CAFO) effluents on gene expression in fish. CAFO effluents contain a variety of agents (growthpromoting hormones, antibiotics, nitrogen, phosphorus, metals) and often find their way into aquatic ecosystems. Several studies have suggested endocrine disruption in fish exposed to CAFO effluents. EERD/NERL plans to examine the effects of CAFO effluents on differential gene expression and endocrine disruption in fish in the Neuse River in North Carolina. The Neuse River is heavily influenced by run-off from both hog and cattle CAFOs. Fathead minnows will be deployed at various locations on the Neuse River, and the fathead minnow gene array being developed in EERD will be used to determine whether gene expression has been altered in those fish. The results of this work will not only provide information as to the effects of CAFO effluents on gene expression in fish, but will also be an initial field validation of the fathead minnow gene array. It is hoped that the gene array can and will be used by EPA Regions, states, tribes, and other monitoring agencies in field applications to screen for EDCs and other pollutants that alter normal gene expression in fish.